

ABSTRACT

The present invention provides a method and system for identifying, designing, and synthesizing proteins and protein backbones. The invention permits the qualitative identification of designable protein configurations and synthesis of protein folds. The method and system involve generating backbone protein configurations using a set of dihedral angle pairs, normalizing the total surface exposure of the configurations; generating a random set of sequences of hydrophobicities with uniform weight on the space of allowed sequences; determining, for each randomly generated sequence, which of the remaining configurations is the ground state; recording a ground-state configuration for each sequence wherein the desirable configurations are those containing the most sequences with that configuration as their ground state and finally, synthesizing sequences of amino acids for the desirable configurations.